

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/825,882

DATE: 11/30/2001
TIME: 12:05:39

Input Set : A:\279152rx.app
Output Set: N:\CRF3\11212001\I825882.raw

ENTERED

11/30/2001
12:05:39

3 <110> APPLICANT: ADLER, JON ELLIOT
 5 <120> TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
 7 <130> FILE REFERENCE: 078003/0279152/RXT
 9 <140> CURRENT APPLICATION NUMBER: 09/825,882
 10 <141> CURRENT FILING DATE: 2001-04-05
 12 <150> PRIOR APPLICATION NUMBER: 60/195,532
 13 <151> PRIOR FILING DATE: 2000-04-07
 15 <150> PRIOR APPLICATION NUMBER: 60/247,014
 16 <151> PRIOR FILING DATE: 2000-11-13
 18 <160> NUMBER OF SEQ ID NOS: 31
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1002
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 30 ttttggatg tagtgaagag gcaggcactg agcaacagtq atttgtgtgct gctgtgtctc 180
 31 agcatcagcc ggctttcct gcatggactg ctgttccatgat gtgctatcca gcttaccac 240
 32 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 300
 33 attgcaaacc aagccaaacct ctggcttgct gcctgcctca gcctgcctta ctgctccaag 360
 34 ctcatccgtt tctctcacac cttectgatc tgcttggcaa gctgggtctc caggaagatc 420
 35 tcccagatgc tcctggatatttcttcatc tcctgcattc gactgtctt ctgtgtttgg 480
 36 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca 540
 37 aggctcaact ggcagattaa agatctcaat ttattttatt ctttcttctt ctgctatctg 600
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 39 ggaaggcaca tgaggacaat gaaggcttat accagaaaact ctcgtgaccc cagcctggag 720
 40 gcccacatta aagccctcaa gtcctttgtc tcctttttt gcttctttgt gatatcatcc 780
 41 tgtgttgctt tcacatctgt gcccctactg attctgtggc gcgacaaaat aggggtgatg 840
 42 gtttgtgttq ggataatggc agcttgcctt tctggcatg cagccatctt gatctcaggc 900
 43 aatgccaagt tgaggagagc tgtgtatgacc attctgtctt gggctcagag cagcctgaag 960
 44 gtaagagccg accacaaggc agattcccg acactgtgct ga 1002
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 48 <211> LENGTH: 333
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 2
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 55 Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
 56 20 25 30
 57 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
 58 35 40 45
 59 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 60 50 55 60
 61 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
 62
 63
 64
 65

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68	Phe	Gln	Lys	Leu	Ser	Glu	Pro	Leu	Asn	His	Ser	Tyr	Gln	Ala	Ile	Ile
69							85			90					95	
71	Met	Leu	Trp	Met	Ile	Ala	Asn	Gln	Ala	Asn	Leu	Trp	Leu	Ala	Ala	Cys
72								100			105				110	
74	Leu	Ser	Leu	Leu	Tyr	Cys	Ser	Lys	Leu	Ile	Arg	Phe	Ser	His	Thr	Phe
75								115			120				125	
77	Leu	Ile	Cys	Leu	Ala	Ser	Trp	Val	Ser	Arg	Lys	Ile	Ser	Gln	Met	Leu
78								130			135				140	
80	Leu	Gly	Ile	Ile	Leu	Cys	Ser	Cys	Ile	Cys	Thr	Val	Leu	Cys	Val	Trp
81	145							150				155				160
83	Cys	Phe	Phe	Ser	Arg	Pro	His	Phe	Thr	Val	Thr	Thr	Val	Leu	Phe	Met
84								165			170				175	
86	Asn	Asn	Asn	Thr	Arg	Leu	Asn	Trp	Gln	Ile	Lys	Asp	Leu	Asn	Leu	Phe
87								180			185				190	
89	Tyr	Ser	Phe	Leu	Phe	Cys	Tyr	Leu	Trp	Ser	Val	Pro	Pro	Phe	Leu	Leu
90								195			200				205	
92	Phe	Leu	Val	Ser	Ser	Gly	Met	Leu	Thr	Val	Ser	Leu	Gly	Arg	His	Met
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96	225							230				235				240
98	Ala	His	Ile	Lys	Ala	Leu	Lys	Ser	Leu	Val	Ser	Phe	Phe	Cys	Phe	Phe
99								245			250				255	
101	Val	Ile	Ser	Ser	Cys	Val	Ala	Phe	Ile	Ser	Val	Pro	Leu	Ile	Leu	
102								260			265				270	
104	Trp	Arg	Asp	Lys	Ile	Gly	Val	Met	Val	Cys	Val	Gly	Ile	Met	Ala	Ala
105								275			280				285	
107	Cys	Pro	Ser	Gly	His	Ala	Ala	Ile	Leu	Ile	Ser	Gly	Asn	Ala	Lys	Leu
108								290			295				300	
110	Arg	Arg	Ala	Val	Met	Thr	Ile	Leu	Leu	Trp	Ala	Gln	Ser	Ser	Leu	Lys
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124	tttagcgttt	tacttgctga	ataccttcatt	ggtatcattg	caaatggttt	catcatggct	120									
125	atacatgcag	ctgaatgggt	tcaaaaataaq	qcagtttcca	caagtggcag	gatctgggtt	180									
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127	tcaacccccc	taagttttta	ttctgaagac	gctgtatatt	atgcattcaa	aataagttt	300									
128	atattcttaa	atttttgtag	cctgtggttt	gctgcctggc	tcagtttctt	ctactttgt	360									
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131	aacatctgca	ctgtgtattt	taacaattct	ttccctatcc	actcctccaa	ctccactaag	540									
132	aaaacatact	tgtctgagat	caatgtggtc	ggtctggctt	ttttcttaa	cctggggattt	600									
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134 cacaccctac acatgggaag caatgccaca gggtccaacg accccagcat ggaggctcac 720
 135 atgggggcca tcaaagctat cagctactt ctcattctct acattttcaa tgcaagtgc 780
 136 ctgttatct acctgtccaa catgttgac atcaacagtc tgtgaaataa tttgtccag 840
 137 atcatcatgg ctgcctaccc tgccagccac tcaattctac tgattcaaga taaccctggg 900
 138 ctgagaagag cctggaagcg gcttcagctt cgacttcatac tttacccaaa agagtggact 960
 139 ctgtga 966
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 151 Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly Ile
 152 20 25 30
 154 Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val Gln
 155 35 40 45
 157 Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
 158 50 55 60
 160 Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
 161 65 70 75 80
 163 Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
 164 85 90 95
 166 Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
 167 100 105 110
 169 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
 170 115 120 125
 172 Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
 173 130 135 140
 175 Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
 176 145 150 155 160
 178 Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
 179 165 170 175
 181 Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
 182 180 185 190
 184 Ala Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
 185 195 200 205
 187 Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
 188 210 215 220
 190 Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
 191 225 230 235 240
 193 Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
 194 245 250 255
 196 Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
 197 260 265 270
 199 Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
 200 275 280 285
 202 Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
 203 290 295 300

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205 Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
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208 Leu
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213 <211> LENGTH: 972
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 5
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220 gccatctatg gggtcgatgt ggcaggggc aaaacactcc ccactggta ccgcattatg 180
221 ttgtatgttgc gctttccag gctcttgcta cagatttgaa tgatgttgttga gaacatttc 240
222 aatctgttatc tccgaatttgt ttataaccaa aactcagtgt atatcctctt caaagtcatc 300
223 actgtctttc tgaaccattc caatctctgg tttgtgcct ggctcaaagt cttcttattgt 360
224 ctttagaatttgc caaacttcaa tcatttcatttgc ttcttcgttga tgaagaggaa aatcatatgt 420
225 ctgtatgcctt ggcttctcag gctgtcagtg ttgggttcct taagcttcag ctttcctctc 480
226 tcgagagatg tcttcaatgt gtatgtgaat agctccattc ctatcccctc ctccaactcc 540
227 aegggagaaga agtacttctc tgagaccaat atggtaacc tggtattttt ctataacatg 600
228 gggatcttcg ttcctctgtat catgttcattc ctggcagccca ccctgtctgat cctctctctc 660
229 aagagacaca ccctacacat gggaaagcaat gccacagggt ccagggaccc cagcatgaag 720
230 gtcacatag gggccatcaa agccaccagg tactttctca tcctctacat tttcaatgca 780
231 attgctctat ttcttccac gtccaaatc tttgacactt acagttctg gaatattttg 840
232 tqcaagatca tcattggctgc ctaccctgcc ggccactcag tacaactgat cttgggcaac 900
233 cctggctgtga gaagacccgtt gaagcggtt cagcaccaag ttcctcttta cctaaaagg 960
234 cagactctgtt ga 972
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 323
239 <212> TYPE: PRT
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246 Lys Val Thr Phe Thr Leu Val Val Ser Gly Ile Glu Cys Ile Thr Gly
247 20 25 30
249 Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
250 35 40 45
252 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
253 50 55 60
255 Phe Ser Arg Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
256 65 70 75 80
258 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
259 85 90 95
261 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
262 100 105 110
264 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
265 115 120 125
267 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
268 130 135 140
270 Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu

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271 145           150           155           160
273 Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
274           165           170           175
276 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
277           180           185           190
279 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
280           195           200           205
282 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
283           210           215           220
285 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
286           225           230           235           240
288 Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
289           245           250           255
291 Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
292           260           265           270
294 Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
295           275           280           285
297 Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
298           290           295           300
300 Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
301           305           310           315           320
303 Gln Thr Leu
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308 <211> LENGTH: 930
309 <212> TYPE: DNA
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315 atctcctttg ctgaccaaattt totcaactgtc ctggcggtct ccagagttgg tttgtctgg 180
316 gtattattat taaactggta ttcaactgtc ttgaatccag cttttaatag tgtagaagta 240
317 agaactactg cttataatat ctgggcagtg atcaaccatt tcagcaactg gcttgctact 300
318 accctcagca tattttatattt gctcaagattt gccaattttt ccaactttat ttttcttcac 360
319 ttaaaggagga gagttaaagag tgcattctg gtgtatgttggggcctt gctattttt 420
320 gcttgtcatc ttttgttat aaacatgaat gagattgtgc ggacaaaaga atttgaagga 480
321 aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcaaatat gactgtaacc 540
322 atggtagcaa acttagtacc cttcaactctg accctactat cttttatgtt gttaatctgt 600
323 tctttgtgtaa acatctcaa gaagatgcag ctccatggta aaggatctca agatcccagc 660
324 accaagggtcc acataaaaagc tttgcaaaact gtgtatctcct tcctcttgc atgtgccatt 720
325 tactttctgt ccataatgtat atcagtttg agttttggaa gtctggaaaa caaacctgtc 780
326 ttcatgttct gcaaagctat tagattcagc tatccttcaa tccacccatt catcctgatt 840
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328 gtgaaaggag agaagacttc atctccatag                               930
331 <210> SEQ ID NO: 8
332 <211> LENGTH: 309
333 <212> TYPE: PRT
334 <213> ORGANISM: Homo sapiens
336 <400> SEQUENCE: 8
337 Met Ile Thr Phe Leu Pro Ile Phe Ser Ser Leu Val Val Val Thr

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30